

1000 800 600 400 200 0

Fig. 1



K-D

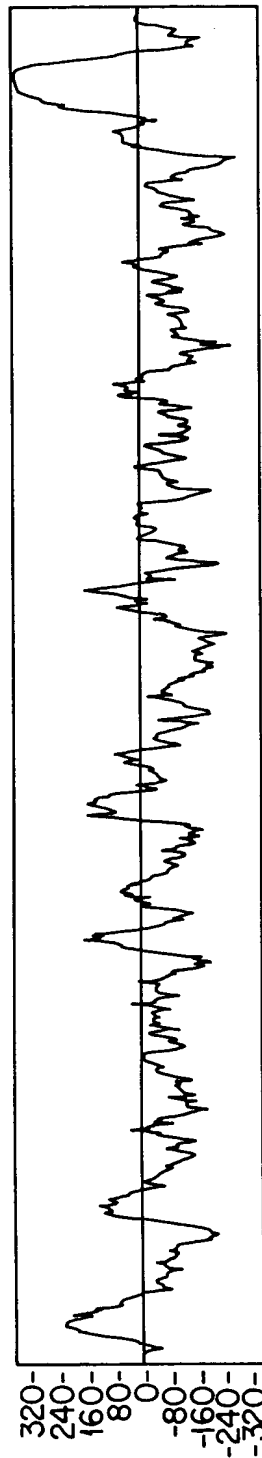


Fig. 2A

MMP-11	MAPAAWLRSA	AARALLPPML	LLLLQPPPL-	-----	-----LARA	33
MMP-1	MHS-----	-----FPPL	LLLLFWGVVS	HSFPATLETQ	EQDVDLVQKY	37
MMP-8	MFSLKTL---	-----PFL	LLLVHQISKA	FPVSSKERNT	KTVQD-----Y	36
MMP-10	MMHL-----	-----AFL	VLLCLPVCSA	YPLSGAAKEE	DSNKDLAQOY	37
MMP-3	MKSL-----	-----PIL	LLLCVAVCSA	YPLDGAARGE	DTSMNLVQKY	37
MMP-9	MSLWQP----	---LVLVLLV	LGCCFAAPRQ	RQSTLVLFPG	DLRTNLTDRQ	43
MMP-2	-----	-----	-----AP--	--SPIIKFPG	DVAPK-TDKE	19
MMP-7	MR-----	---LTVLCAV	CLLPGLALP	LPQEAGGMSE	-----LQWE	33
MT-MMP	MSPAP-----	-----RPSR	CLLLPLLTIG	TALASLGSQAQ	SSSFS-PEAW	38
Consensus	M...-----	-----P.L	LLL.....	50
MMP-11	LPPDVHHL--	---HAERR-G	PQPWHAALPS	SP---APAPA	TQEAPRRPASS	74
MMP-1	L-EKYYNLKN	DGRQVEKRRN	SGPVVEKLKQ	MQEFFGLKVT	GKPDAAETLKV	86
MMP-8	L-EKFYQLPS	NQYQSTRKNG	TNVIVEKLKE	MQRFFGLNVT	GKPNREETLDM	85
MMP-10	L-EKYYNLEK	DVKQFRRK-D	SNLIVKKIQG	MQKFLGLEVT	GKLDTDTEV	85
MMP-3	L-ENYYDLKK	DVKQFVRRKD	SGPVVKKIRE	MQKFLGLEVT	GKLDSDTLEV	86
MMP-9	LAEEYLYRYG	YTRVAEMRGE	SKSLGPALLL	LQKQLSLPET	GELDSATLKA	93
MMP-2	LAVQYLNTF-	YGCPE-SCN	LFVLKDTLKK	MQKFFGLPQT	GDLDQNTIET	67
MMP-7	QAQDYLKRF-	YLYDSETK-N	ANSLEAKLKE	MQKFFGLPIT	GMLNSRVIEI	81
MT-MMP	L-QQGYLPP	GDLRTHTQRS	PQSLSAIAA	MQKFGYGLQVT	GKADADTMKA	87
Consensus	L-E.Y..I..E....KL..	MQKF.GL.VT	GKLD..TL..	100

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Fig. 2B

MMP-11	LRPPRCGVPD	-PSDGLSARN	RQKRFVLSGG	RWEKTDLTyr	ILRFPWQLVQ	123
MMP-1	MKQPRCGVPD	-VAQ-FVL--	----TE-GNP	RWEQTHLTyr	IENYTPDLPR	127
MMP-8	MKKPRCGVPD	-SGG-FML--	----TP-GNP	KWERTNLTyr	IRNYTPQLSE	126
MMP-10	MRKPRCGVPD	-VGH-FSS--	----FP-GMP	KWRKTHLTyr	IVNYTPDLPR	126
MMP-3	MRKPRCGVPD	-VGH-FRT--	----FP-GIP	KWRKTHLTyr	IVNYTPDLPK	127
MMP-9	MRTPRCGVPD	-LGR-FQT--	----FE-GDL	KWHHNNITYW	IONYSEDLPK	134
MMP-2	MRKPRCGNPD	-VAN-YNF--	----FP-RKP	KWDKNQITYR	IIGYTPDLDP	108
MMP-7	MQKPRCGVPD	-VAE-YSL--	----FP-NSP	KWTSKVVTyr	IVSYTRDLPH	122
MT-MMP	MRRPRCGVPD	KFGAEIKANV	RRKRYAIOGL	KWQHNEITFC	IQNYTPKVGE	137
Consensus	MRKPRCGVPD	-VG.-F.--	----FP-G.P	KW..T.LTyr	I.NYTPDLP.	150

MMP-11	EQVRQTMAEA	LKVWSDVTPL	TFTEV-----	---HEGRADI	MIDFARYWDG	165
MMP-1	ADVDDHAIEKA	FQLWSNVTPPL	TFTKV-----	---SEGQADI	MISFVRGDHR	169
MMP-8	AEVERAIKDA	FELWSVASPL	IFTRI-----	---SQGEADI	NIAFYQRDHG	168
MMP-10	DAVDSAIEKA	LKVWEEVTPL	TF SRL-----	---YEGEADI	MISFAVKEHG	168
MMP-3	DAVDSAVEKA	LKVWEEVTPL	TF SRL-----	---YEGEADI	MISFAVREHG	169
MMP-9	AVIDDAFARA	FALWSAVTPL	TFTRV-----	---YSRDADI	VIQFGVAEHG	176
MMP-2	ETVDDAFARA	FQVWSDVTPL	RFSRI-----	---HDGEADI	MINFGRWEHG	150
MMP-7	ITVDRILVSKA	LNWVGKEIPL	HFRKV-----	---VWGTDADI	MIGFARGAHG	164
MT-MMP	YATYEAIRKA	FRVWESATPL	RFREVPYAYI	REGHEKQADI	MIFFAEGFHG	187
Consensus	..VD.A..KA	F.VWS.VTPL	TF.RV-----	---.EG-ADI	MI.FA...HG	200

MMP-11	DDLPEFGPGG	ILAHAFPPKT	HREGDVHFDY	DETWIGDDQ	GTD-----	208
MMP-1	DNSPFDGPGG	NLAHAFQPGP	GIGGDAHFE	DERWTNNFT-	EYN-----	211
MMP-8	DNSPFDGPGG	ILAHAFQPGQ	GIGGDAHFDA	EETWTNTSA-	NYN-----	210
MMP-10	DFYSEFDGPGH	VLAHAYPPGP	GLYGD IHFDD	DEKWTEDAS-	GTN-----	210
MMP-3	DFYSEFDGPGN	VLAHAYAPGP	GINGDAHFD	DEQWTKDTT-	GTN-----	211
MMP-9	DGYPFDGKDG	LLAHAFPPGP	GIQGD AHFDD	DELWSLGK-	VVPTTRFGNA	225
MMP-2	DGYPFDGKDG	LLAHAFAPGT	GVGDSHFDD	DELWTLGEG-	QVVRVKYGNA	199
MMP-7	DSYPFDGPGN	TLAHAFAPGT	GLGDAHFE	DERWTDGSSL	GIN-----	207
MT-MMP	DSTPFDEGEG	FLAHAYFPGP	NIGGDTHFDS	AEPWTVRNE-	DLN-----	229
Consensus	D.YPFDEGPGG	.LAHAF.PGP	GIGGDAHFD.	DE.WT....-	.N-----	250

MMP-11	-----	-----	-----	-----	-----	208
MMP-1	-----	-----	-----	-----	-----	211
MMP-8	-----	-----	-----	-----	-----	210
MMP-10	-----	-----	-----	-----	-----	210
MMP-3	-----	-----	-----	-----	-----	211
MMP-9	DGAACHFPFI	FEGRSYSACT	TDGRSDGLPW	CSTANYDTD	DRFGFCPSER	275
MMP-2	DGEYCKFPFL	FNGKEYNSCT	DTGRSDGFLW	CSTYNFEKD	GKYGFCPHEA	249
MMP-7	-----	-----	-----	-----	-----	207
MT-MMP	-----	-----	-----	-----	-----	229
Consensus	-----	-----	-----	-----	-----	300

[illegible]

MMP-11	--	--	--	--	--	--
MMP-1	--	--	--	--	--	--
MMP-8	--	--	--	--	--	--
MMP-10	--	--	--	--	--	--
MMP-3	--	--	--	--	--	--
MMP-9	FGFCPTRADS	TVMGGSAGE	LCVFPFTFLG	KEYSTCTSEG	RGDGRWLCAT	208
MMP-2	YGFCPETAMS	TVGG-NSEGA	PCVFPFTFLG	NKYESCTSAG	RSDGKMWCAT	211
MMP-7	--	--	--	--	--	210
MT-MMP	--	--	--	--	--	210
Consensus	----	----	----	----	----	211
						375
						348
						207
						229
						400

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Fig. 2E

MMP-11	-----	-----L	LQVAA-HEFG	HVLGLQHTTA	AKALMSAFY-	237
MMP-1	-----	-----L	HRVAA-HELG	HSLGLSHSTD	IGALMYPSTY-	240
MMP-8	-----	-----L	FLVAA-HEFG	HSLGLAHSSD	PGALMYPNY-	239
MMP-10	-----	-----L	FLVAA-HELG	HSLGLFHSAN	TEALMYPLYN	240
MMP-3	-----	-----L	FLVAA-HEIG	HSLGLFHSAN	TEALMYPPIYH	241
MMP-9	TSNFDSDKKW	GFCPDQGYSL	FLVAA-HEFG	HALGLDHSSV	PEALMYPMY-	423
MMP-2	TANYDDDRKW	GFCPDQGYSL	FLVAA-HEFG	HAMGLEHSQD	PGALMAPIY-	396
MMP-7	-----	-----	FLYAATHELG	HSLGMGHSSD	PNAVMPPTY-	236
MT-MMP	-----	-----GNDI	FLVAV-HELG	HALGLEHSSD	PSAIMAPFY-	261
Consensus	-----	-----L	FLVAA-HE.G	HSLGL.HS.D	P.ALMYP.Y-	450

MMP-11	TF--RYPLSL	SPDDCRGVQH	LYG-----	-----	-----	258
MMP-1	TF--SGDVQL	AQDDIDGIQA	IYG-----	-----	-----	261
MMP-8	AFRETSNYSL	PQDDIDGIQA	IYG-----	-----	-----	262
MMP-10	SFTELAQFRL	SQDDVNGIQS	LYG-----	-----	-----	263
MMP-3	SLTDLTRFRL	SQDDINGIQS	LYG-----	-----	-----	264
MMP-9	RF--TEGPPL	HKDDVNGIRH	LYGPRPEPEP	RPPTTTTPQP	TAPPTVCPTG	471
MMP-2	TY--TKNFRL	SQDDIKIGIQE	LYG-----	-----	-----	417
MMP-7	GNGDPQNFKL	SQDDIKIGIQK	LYGKRSNSRK	K-----	-----	267
MT-MMP	QWMDTENFVL	PDDRRRGIQQ	LYGSEGFPT	KMPQPRTTS	RPSVPDKPKN	311
Consensus	.F.....F.L	SQDDI.GIQ.	LYG-----	-----	-----	500

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Fig. 2F

MMP-11	-----	-----QPW	PTVTSRTPAL	GPQAGIDTNE	IAPLEPDAPP	291
MMP-1	-----	-----	RSQNPVQP-I	GPQTP-----	-----KAC	278
MMP-8	-----	-----	----LSSNP-I	QPTGP---ST	P-----KPC	279
MMP-10	-----	-----P	PPASTEPEP-L	VPTKS---VP	S-GSEMPAKC	289
MMP-3	-----	-----P	PPDSPETP-L	VPTEP---VP	P-EPGTPANC	290
MMP-9	PPTVHPSERP	TAGPTGPPSA	GPTGPPTA-G	PSTAT---TV	PLSPVD-DAC	516
MMP-2	-----	-----	---ASPD I-D	LGTGP---TP	TLGPVTPEIC	440
MMP-7	-----	-----	-----	-----	-----	267
MT-MMP	PTYGPNICDG	NFDTVAMLRG	EMFVFKRRWF	WVRNNOQVMD	GYPMPIGQFW	361
Consensus	-----	-----P-.	.PT.....C	550

MMP-11	DACEASFDAV	STIR-GELFF	FKAGFVWRLR	GGQL-QPGYP	ALASRHWQGL	339
MMP-1	DS-KLTFDAI	TTIR-GEVME	FKDRFYMR-T	NPFY-PEVEL	NFTSVFWPQL	324
MMP-8	DP-SLTFDAI	TTLR-GEILF	FKDRYFWR-R	HPQL-QRVEM	NFISLFWPSL	325
MMP-10	DP-ALSFDAI	STLR-GEYLF	FKDRYFWR-R	SHWN-PEPEF	HLISAFWPSL	335
MMP-3	DP-ALSFDAV	STLR-GEILI	FKDRHFWR-K	SLRK-LEPEL	HLISSFWPSL	336
MMP-9	NV-NI-FDAI	AEIG-NQLYL	FKDGKYWRFS	EGRGSRPQGP	FLIADKWPAL	563
MMP-2	KQ-DIVFDGI	AQIR-GEIFF	FKDRFIWRTV	TPRD-KPMGP	LLVATFWPEL	487
MMP-7	-----	-----	-----	-----	-----	267
MT-MMP	RGLPASINTA	YERKDCKEVE	FKGDKHWVFD	EASLEPGYPK	HIKELGRG-L	410
Consensus	D.-...FDAI	.T.R-GE..F	FKDR..WR-L.S.FWP.L	600

MMP-11	VPSE--IDAA	FQDADGYAYF	LRRLYWKFD	PVKVKALEGF	PRIV-----	473
MMP-1	GIGH--KVDA	V--FMKDGEF	-----YF-FH	GTRQYKFDPK	TKRILTLQ--	458
MMP-8	GIES--KVDA	V--FQEHFF	-----HV-FS	GPRYAFDLI	AQRVTRVA--	456
MMP-10	GVEP--KVDA	V--LQAFGFF	-----YF-FS	GSSQFEFDPN	ARMVTHIL--	468
MMP-3	GIDS--KIDA	V--FEEFGFF	-----YF-FT	GSSQLEFDPN	AKKVTHTL--	469
MMP-9	GVPL--DTHD	VFQYREKAYF	---CQDR-FY	WRVSSRSEIN	QVDQVGYV--	697
MMP-2	AIPD--NLDA	VVDLQGGG--	-----HS-YF	FKGAYYIKLE	N-QSLKSVKF	621
MMP-7	-----	-----	-----	-----	-----	267
MT-MMP	SGRPDEGTE	EETEVIIEV	DEEGGAVSA	AAVLPVLLL	LLVLAUGLAV	559
Consensus	G.....DA	V.....F	-----F.	750

MMP-11	---GPD-FFG	CAE-----PA	NTFLX----	-----	-----	489
MMP-1	---KANSWFN	CR-----KN	-----	-----	-----	469
MMP-8	---RGNKWLN	CRY-----GX	-----	-----	-----	468
MMP-10	---KNSWLH	C-----	-----	-----	-----	476
MMP-9	---TYD-ILQ	CPE-----DX	-----	-----	-----	477
MMP-2	GSIKSD-WLG	C-----	-----	-----	-----	708
MMP-7	-----	-----	-----	-----	-----	267
MT-MMP	FFRRRHGTPR	RLLYCQRSL	DKV-----	-----	-----	582
Consensus	-----WL.	C-----	-----	-----	-----	796

Fig. 3

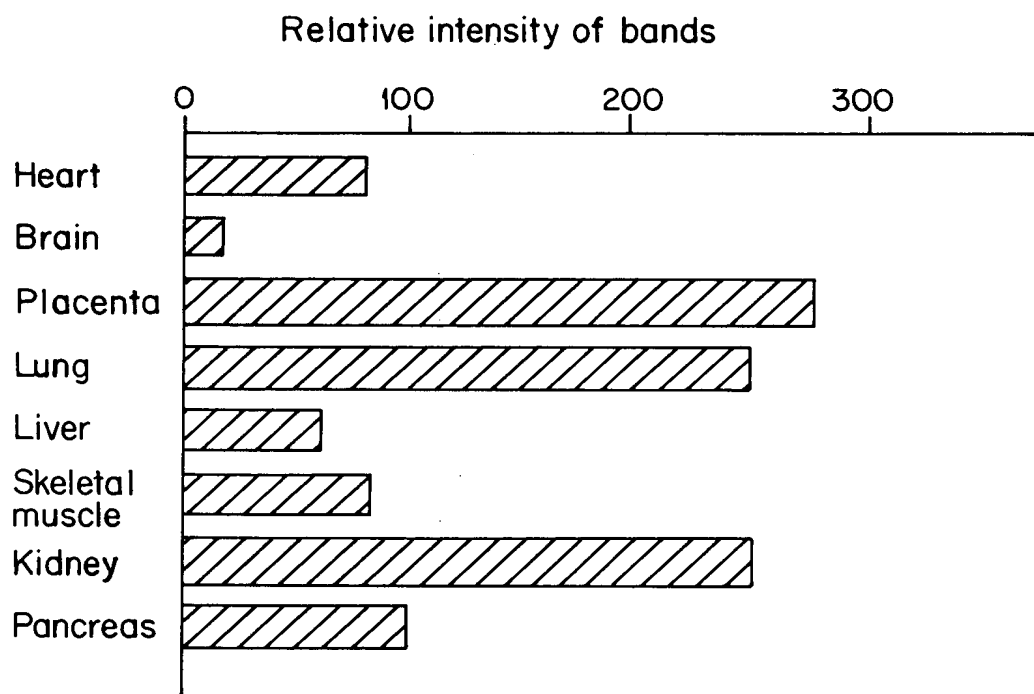


Fig. 4

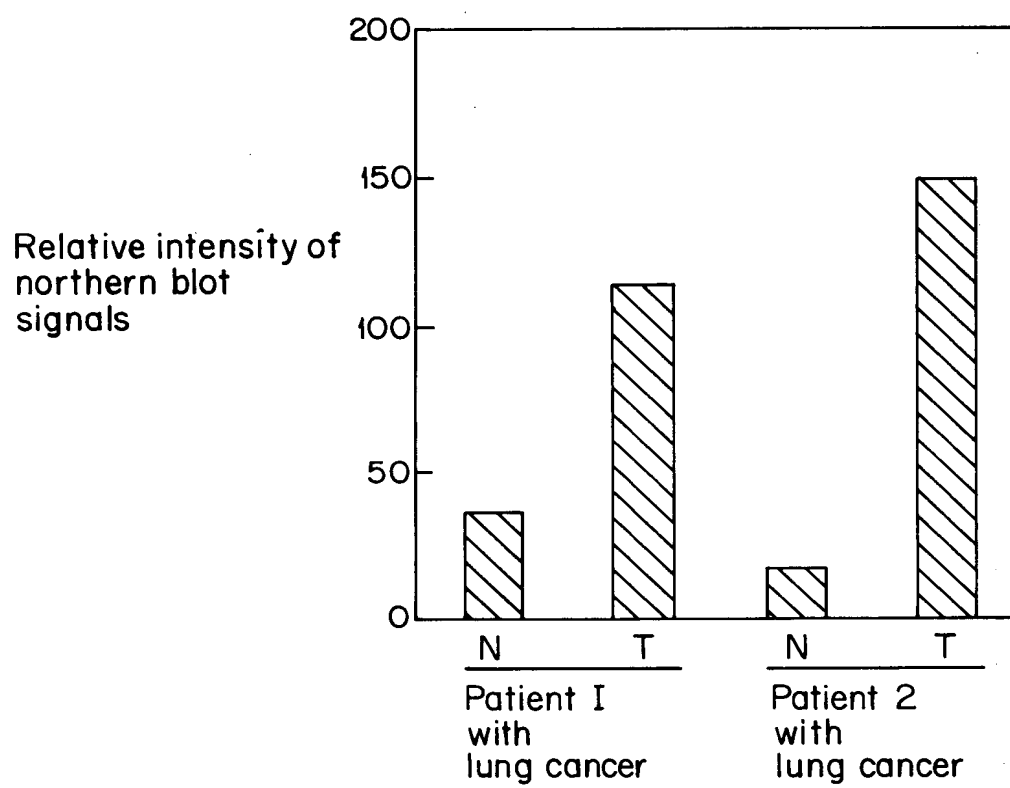


Fig. 5

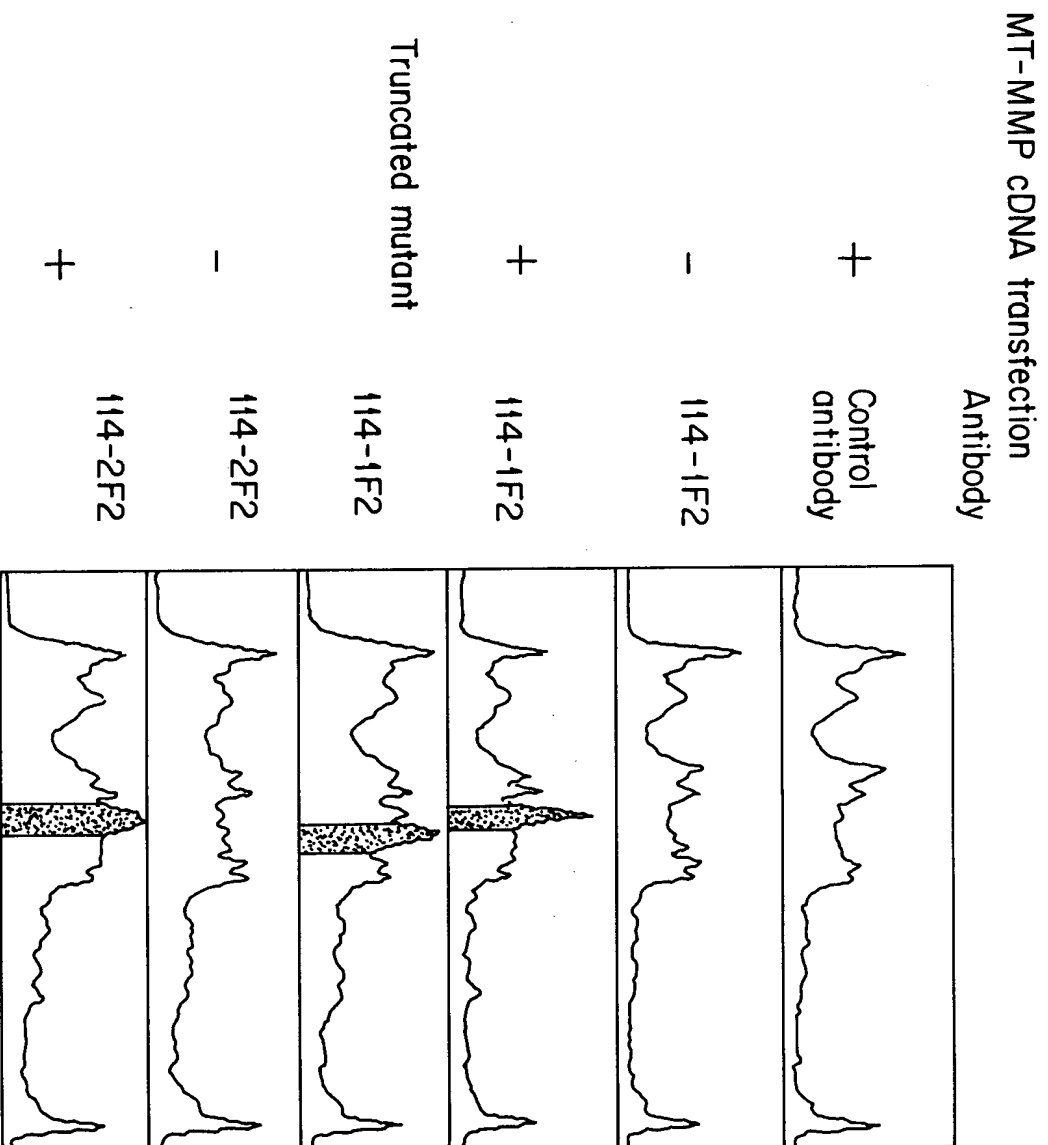


Fig. 6

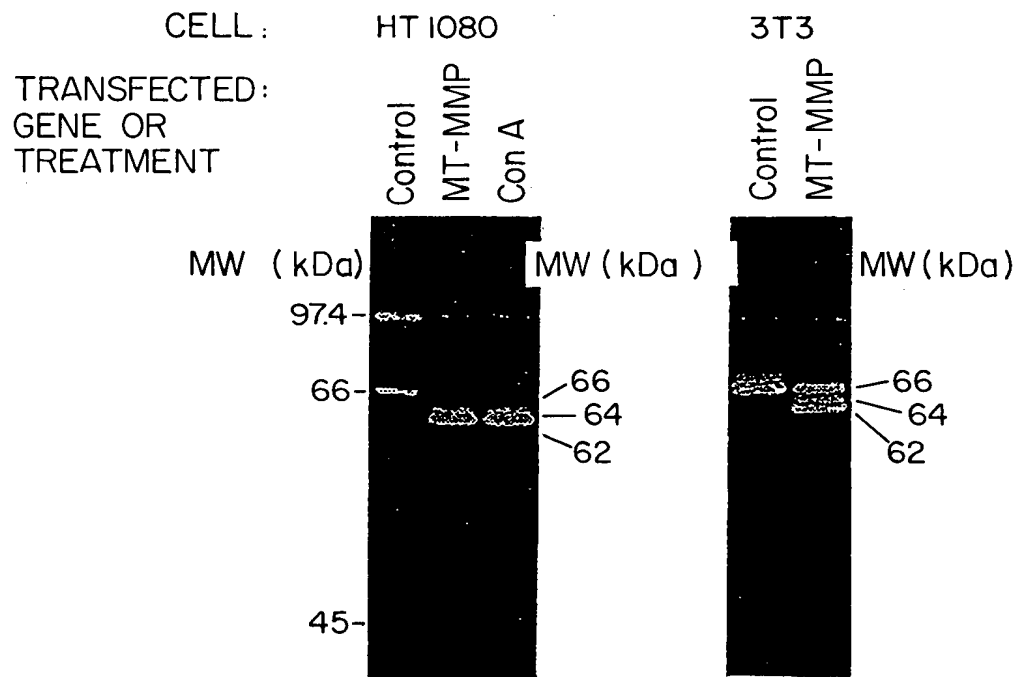


Fig. 7

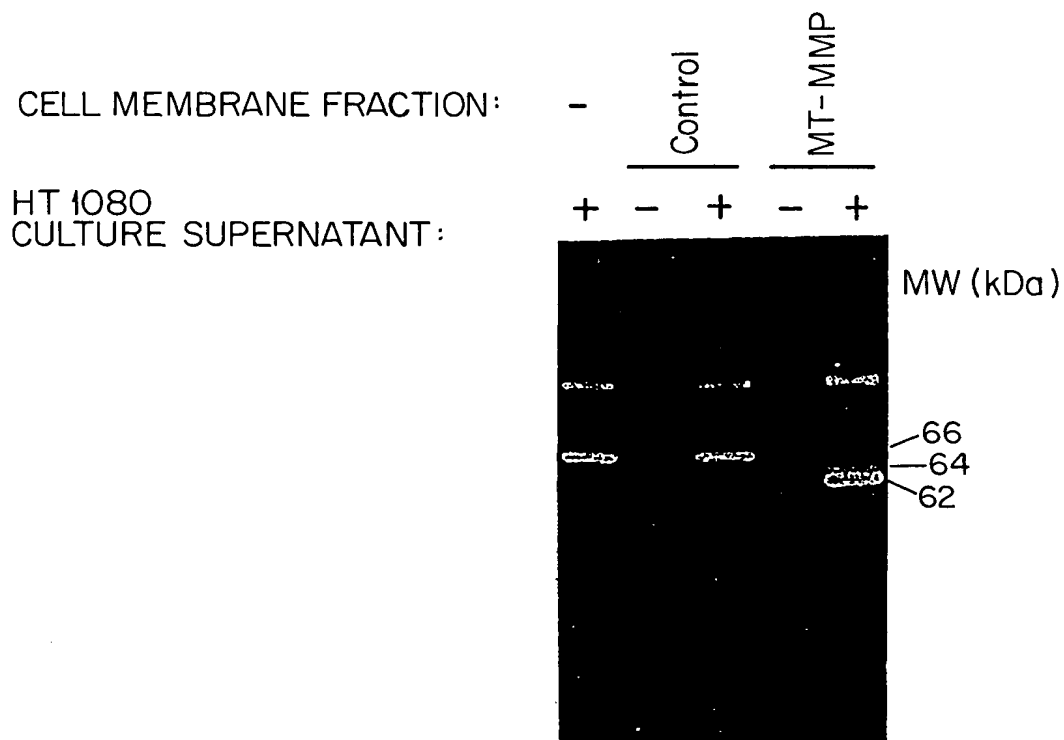


Fig. 8

